

TeDench

**RAW SEQUENCE LISTING
ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



RECEIVED

NOV 29 2000

TECH CENTER 1600/2900

DH/18

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/555,981

Source: 1642

Date Processed by STIC: 11/16/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/555,981

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

RECEIVED

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

10/20/00

1642

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/555,981
DATE: 11/16/2000
TIME: 19:24:38Input Set : A:\Leadd bl.app
Output Set: N:\CRF3\11162000\I555981.rawDoes Not Comply
Corrected Diskette Needed

see pp. 3-5, too

```
3 <110> APPLICANT: Noteborn, Mathieu Hubertus Maria
4   Danen-Van Oorschot, Astrid Adriana Anna Maria
6 <120> TITLE OF INVENTION: Molecules Interacting with Apoptin
8 <130> FILE REFERENCE: LEBV.006.01
10 <140> CURRENT APPLICATION NUMBER: 09/555,981
11 <141> CURRENT FILING DATE: 1998-12-03
13 <150> PRIOR APPLICATION NUMBER: PCT/NL98/00687
14 <151> PRIOR FILING DATE: 1998-12-03
16 <150> PRIOR APPLICATION NUMBER: 97203781.6 EP
17 <151> PRIOR FILING DATE: 1997-12-03
19 <160> NUMBER OF SEQ ID NOS: 13
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 658
25 <212> TYPE: DNA
26 <213> ORGANISM: Apoptin-Associating Clone
28 <400> SEQUENCE: 1
29 ggggggatcat ggaagctgat aaagatgaca cacaacaaat tcttaaggag cattcgccag 60
30 atgaatttat aaaagatgaa caaaataaag gactaattga tgaattaca aagaaaaata 120
31 ttcaactaaa gaaggagatc caaaagcttg aaacggagtt acaaggagct accaaagaat 180
32 tccagattaa agaggatatt cctgaaacaa agatgaaatt cttatcagtt gaaactcctg 240
33 agaatgacag ccagttgtca aatatctcct gtctgtttca agtgagctcg aaagtctctt 300
34 atgagatata aaaaggacaa gcaattatca cctttgaaaa agaagaagtt gctcaaaatg 360
35 tggtaagcat gagtaaacat catgtacaga taaaagatgt aaatctggag gttacggcca 420
36 agccagttcc attaaattca ggagtcagat tccaggttta tgtagaagtt tctaaaatga 480
37 aaatcaatgt tactgaaatt cctgacacat tgcgtgaaaa tcaaatgaga gacaaactag 540
W--> 38 agctgagctt ttcaaaagtc cgaatggga ggcggagag tggaccgcgt gggactatga 600
W--> 39 cagacagtcg gggagtgag tcatcacgtt tggnggagat tgggagtgge tgacannn 658
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 717
44 <212> TYPE: DNA
45 <213> ORGANISM: Apoptin-Associating Clone
47 <400> SEQUENCE: 2
48 cggagttaca agaggtacc aaagaattcc agattaaaga ggatattcct gaaacaaaga 60
W--> 49 tgaattctt atcagttgaa actcctgana atgacagcca gttgtcaa atctcctggt 120
50 cgtttcaagg tgagctcgaa agttccttat gagatacaaa aaggacaatg cacttatcac 180
W--> 51 ctttgaaaaa ggaagaagtt gctcaaaatg tngtaagca tgagtaaaac tcatgtacag 240
52 ataataagat gtaaatctgg aggttacggc caaagccaaag ttccattaat attcaaggag 300
W--> 53 tcangattcc agngttatgc tagaangttt ctaaaaatga naatcaatgg ttactggaaa 360
W--> 54 ttcttgagca cattgcgntg aaagatcaag atgacgaaga caaactaaga agctgagctt 420
W--> 55 ttcaaaagtc ccgaaanatg gaagagcggg agagggtggn accgcgtgng anctatgaca 480
W--> 56 agacaagnc ggggaagntg cagtccatca cgtttgtngg aagattggan gtnggctgac 540
W--> 57 caangaattt tgaaaaagga gangaattac cctctttan gagtaanatc aaaaccctgc 600
W--> 58 cataanaagt tnaactggtt cnccattac acagnantta cannttganc aanantannc 660
W--> 59 aggataattt ncaggggaan aatctnaagn atggcaagnt gacttctgga caanggt 717
62 <210> SEQ ID NO: 3
63 <211> LENGTH: 219
```

see item 10 on
Erra Summary
Sheet

see item 10

RAW SEQUENCE LISTING DATE: 11/16/2000
 PATENT APPLICATION: US/09/555,981 TIME: 19:24:38

Input Set : A:\Leadd b1.app
 Output Set: N:\CRF3\11162000\I555981.raw

```

64 <212> TYPE: PRT
65 <213> ORGANISM: Apoptin-Associating Clone
67 <400> SEQUENCE: 3
68 His Glu Gly Arg Gly Ile Met Glu Ala Asp Lys Asp Asp Thr Gln Gln
69   1           5           10           15
71 Ile Leu Lys Glu His Ser Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn
72           20           25           30
74 Lys Gly Leu Ile Asp Glu Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys
75           35           40           45
77 Glu Ile Gln Lys Leu Glu Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe
78           50           55           60
80 Gln Ile Lys Glu Asp Ile Pro Glu Thr Lys Met Lys Phe Leu Ser Val
81   65           70           75           80
83 Glu Thr Pro Glu Asn Asp Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe
84           85           90           95
86 Gln Val Ser Ser Lys Val Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu
87           100          105          110
89 Ile Thr Phe Glu Lys Glu Glu Val Ala Gln Asn Val Val Ser Met Ser
90           115          120          125
92 Lys His His Val Gln Ile Lys Asp Val Asn Leu Glu Val Thr Ala Lys
93           130          135          140
95 Pro Val Pro Leu Asn Ser Gly Val Arg Phe Gln Val Tyr Val Glu Val
96 145           150           155           160
98 Ser Lys Met Lys Ile Asn Val Thr Glu Ile Asp Asp Thr Leu Arg Glu
99           165          170          175
101 Asp Gln Met Arg Asp Lys Leu Glu Leu Ser Phe Ser Lys Ser Arg Asn
102           180          185          190
104 Gly Arg Arg Arg Cys Gly Pro Arg Gly Thr Met Thr Asp Ser Pro Gly
105           195          200          205
107 Val Gln Ser Ser Arg Leu Val Glu Ile Gly Ser
108           210          215
111 <210> SEQ ID NO: 4
112 <211> LENGTH: 305
113 <212> TYPE: PRT
114 <213> ORGANISM: Apoptin-Associating Clone
116 <400> SEQUENCE: 4
117 Met Glu Ala Asp Lys Asp Asp Thr Gln Gln Ile Leu Lys Glu His Ser
118   1           5           10           15
120 Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn Lys Gly Leu Ile Asp Glu
121           20           25           30
123 Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys Glu Ile Gln Lys Leu Glu
124           35           40           45
126 Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe Gln Ile Lys Glu Asp Ile
127           50           55           60
129 Pro Glu Thr Lys Met Lys Phe Leu Ser Val Glu Thr Pro Glu Asn Asp
130   65           70           75           80
132 Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe Gln Val Ser Ser Lys Val
133           85           90           95
135 Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu Ile Thr Phe Glu Lys Glu

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/555,981 DATE: 11/16/2000
 TIME: 19:24:38

Input Set : A:\Leadd bl.app
 Output Set: N:\CRF3\11162000\I555981.raw

```

136          100          105          110
138 Glu Val Ala Gln Asn Val Val Ser Met Ser Lys His His Val Gln Ile
139          115          120          125
141 Lys Asp Val Asn Leu Glu Val Thr Ala Lys Pro Val Pro Leu Asn Ser
142          130          135          140
144 Gly Val Arg Phe Gln Val Tyr Glu Val Ser Lys Met Lys Ile Asn Val
145 145          150          155          160
147 Thr Glu Ile Pro Asp Thr Leu Arg Glu Asp Gln Met Arg Asp Lys Leu
148          165          170          175
150 Glu Leu Ser Phe Ser Lys Phe Arg Asn Gly Gly Gly Glu Val Asp Arg
151          180          185          190
153 Val Asp Tyr Asp Arg Gln Ser Gly Ser Ala Val Ile Thr Phe Val Glu
154          195          200          205
156 Ile Gly Val Asp Lys Ile Leu Lys Lys Lys Glu Tyr Pro Leu Pro Ile
157          210          215          220
159 Asn Gln Thr Cys His Arg Val Thr Val Ser Pro Tyr Thr Glu Ile His
160 225          230          235          240
162 Leu Lys Lys Tyr Gln Ile Phe Ser Gly Thr Ser Lys Arg Thr Val Leu
163          245          250          255
165 Leu Thr Gly Met Glu Gly Ile Gln Met Asp Glu Glu Ile Val Glu Asp
166          260          265          270
168 Leu Ile Asn Ile His Phe Gln Arg Ala Lys Asn Gly Gly Gly Glu Val
169          275          280          285
171 Asp Val Val Lys Cys Ser Leu Gly Gln Pro His Ile Ala Tyr Phe Glu
172          290          295          300
174 Glu
175 305
178 <210> SEQ ID NO: 5
179 <211> LENGTH: 659
180 <212> TYPE: DNA
181 <213> ORGANISM: Apoptin-Associating Clone
183 <400> SEQUENCE: 5
184 agcagggtgct gcaacaaaag gagcacacga tcaacatgga ggagtgcggg ctgcccgggtgc 60
185 aggtccagcc cttggagctg cccatggtea ccaccatecca ggtgtccagc cagttgagtg 120
186 gccggagggt gttggctact ggatttcttg ccagcctcag gctgagtgag gaggagctgc 180
W--> 187 tggacaanct anagatcttc tttggcaaga ctaggaaagg aggtggcnat gtggacnttc 240
W--> 188 ggganctact gccagggant gtcattgctgg ggtttgctag ggatggagtg gtcancgtc 300
W--> 189 tgtgcaaat cggccatttc acagtgcac tgggtgggca gcanctccct ctgagagttc 360
W--> 190 ctccgtatgt gaatggggan atccagangg ctganatcag gtencagcca nttccccgct 420
191 cggtaactggt gctcaacatt cctgatctct tggatggccc ggagctgcat gacgtcctgg 480
W--> 192 anatccactt ccagaanccc acccgcgggg gcgagatgt aagacgccct gacagtcgta 540
W--> 193 ccccaaggac aacagggcct aacagtcttc acctcctgaa tcaaggctan gggcctcccc 600
W--> 194 cttctcctcc tcccccccc ccccgccaaa ggttctcaan actgggcctg ggctttntg 659
197 <210> SEQ ID NO: 6
198 <211> LENGTH: 631
199 <212> TYPE: DNA
200 <213> ORGANISM: Apoptin-Associating Clone
202 <400> SEQUENCE: 6
203 ccaaagtggc tgagcaggtg ctgcaacaaa aggagcacac gatcaacatg gaggagtgcc 60

```

item 10

RAW SEQUENCE LISTING

DATE: 11/16/2000

PATENT APPLICATION: US/09/555,981

TIME: 19:24:38

Input Set : A:\Leadd bl.app

Output Set: N:\CRF3\11162000\I555981.raw

```

204 ggctgcgggt gcaggtccag cccttggagc tgcccatggt caccaccatc caggtgtcca 120
205 gccagttgag tggccggagg gtgttgggtca ctggatttcc tgccagcctc aggtgagt 180
206 aggaggaagct gctggacaag ctatagatct tctttggcaa gactaggaac ggaagtgagc 240
207 atgtgacagt tcgggagcta ctgccaggga gtgtcatgct ggggtttgct agggatggag 300
W--> 208 tggtcagcg tctgtgcaa atcgccaag ttcacagtgc cactgggtgg gcancaagtc 360
W--> 209 cctctgagag tctctccgta tgtgaatggg gagatccaga aggtgagat caggtcgcan 420
W--> 210 ccagttcccc nctcggtact ggggtgctcaa cttctctgat atcttgatt gggccggagc 480
W--> 211 tgcatacgt cctgganac aactcanaa gccacccgc cggggcngng aggtanaagg 540
W--> 212 cctgacatcn ttaccccaaa ggacagcatg gncctaacag tctcacctc cnaatcangc 600
W--> 213 tnnngggctn cccttctanc ntccccaact g 631

216 <210> SEQ ID NO: 7
217 <211> LENGTH: 629
218 <212> TYPE: DNA
219 <213> ORGANISM: Apoptin-Associating Clone
221 <400> SEQUENCE: 7
222 ggatecactg ccctctgctt qcgagctctg ctctgateac ctttgatgac cccaaagtgg 60
223 ctgagcaggt gctgcaacaa aaggagcaca cgatcaacat ggaggagtgc cggctgcggg 120
224 tgcaggtcca gccctlggag ctgcccatgg tcaccaacct ccaggtgatg gtgtccaaagc 180
W--> 225 canttgagt gcccggagggt gttggtcact ggatttccct ccagctcag gctgantgag 240
W--> 226 gaggagctgc tggacagcta tgagatcttc tttggcaana ctangaacgg angtgccgat 300
227 gtggacgttc gggagctact gccaggaaat gtcagtctgg ggtttgctac ggtatggagt 360
228 gctcagcgtc tgtgccaat cggccagttc acaagtgcca ctgggtgggc agcaagtccc 420
W--> 229 tctgagagtc tctccgtatg tgantggnga gatcagaatg ctganattaa gtcgcatcca 480
W--> 230 attctctgct cnggtactgg tgctcannat cctganatct tggattggcc ccngantnca 540
W--> 231 tganatctgg nagattcaat tncanaagtc canccnnng ncgggaagta nangcccgan 600
W--> 232 anttctnnc ntanggnacg canngcctg 629

235 <210> SEQ ID NO: 8
236 <211> LENGTH: 138
237 <212> TYPE: PRT
238 <213> ORGANISM: Apoptin-Associating Clone
240 <400> SEQUENCE: 8
241 His Glu Gly Pro Lys Val Ala Glu Gln Val Leu Gln Gln Lys Glu His
242 1 5 10 15
244 Thr Ile Asn Met Glu Glu Cys Arg Leu Arg Val Gln Val Gln Pro Leu
245 20 25 30
247 Glu Leu Pro Met Val Thr Thr Ile Gln Val Ser Ser Gln Leu Ser Gly
248 35 40 45
250 Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu Arg Leu Ser Glu
251 50 55 60
253 Glu Glu Leu Leu Asp Lys Leu Glu Ile Phe Phe Gly Lys Thr Arg Asn
254 65 70 75 80
256 Gly Gly Gly Asp Val Asp Val Arg Glu Leu Leu Pro Gly Ser Val Met
257 85 90 95
259 Leu Gly Phe Ala Arg Asp Gly Val Ala Gln Arg Leu Cys Gln Ile Gly
260 100 105 110
262 Gln Val His Ser Ala Thr Gly Trp Ala Ser Ser Pro Ser Glu Ser Leu
263 115 120 125
265 Ser Val Cys Glu Trp Gly Asp Pro Glu Gly
266 130 135

```

10

10

VERIFICATION SUMMARY DATE: 11/16/2000
PATENT APPLICATION: US/09/555,981 TIME: 19:24:40

Input Set : A:\Leadd bl.app
Output Set: N:\CRF3\11162000\I555981.raw

L:38 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:38 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:49 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:49 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:49 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:49 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:49 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:53 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:53 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:53 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:53 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:54 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:54 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:54 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:54 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:55 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:55 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:55 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:55 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:56 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:56 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:56 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:56 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:57 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:57 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:57 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:57 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/555,981

DATE: 11/16/2000

TIME: 19:24:40

Input Set : A:\Leadd bl.app

Output Set: N:\CRF3\11162000\I555981.raw

L:187 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:187 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:187 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:187 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:187 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:188 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:188 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:208 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:225 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:345 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:585 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13